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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Comp
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QWHU0
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T10798
S22052
S52715
A25451
A25451
A33647
JH0529
A34170
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1	T17456	S72273	T31065	S54986	149139	B48232	S42442	T06291	S51939	149681	JU0029	S11674	S22697	S11515	S24407
graphanons teraced	nypothetical prote	actin-depolymerizi	diaphanous protein	regulatory protein	lymphotoxin-beta -	cysteine-rich exte	nuclear protein EB	extensin homolog T	chitinase (EC 3.2.	glyceraldehyde-3-p	tumor necrosis fac	acrosin (EC 3.4.21	extensin - Volvox	formin - mouse	formin isoform IV

ALIGNMENTS

	RESULT 1
	Tag lound - himan
	C; Species: Homosapiens (man)
	C;Date: 29-May-1998 #Sequence_revision 29-May-1998 #text_change 21-Jul-2000 C;Accession: I38707; JC2340; S57565; I38554
	R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S. Int. Immunol. 6, 1567-1574, 1994
	A;Title: Human Fas ligand: gene structure, chromosomal location and species specific: A;Reference number: I38707; MUID:95127560
	A; Status: preliminary; translated from GB/EMBL/DDBJ
	A; MOLECULE Type: mknA
ave a	A;Cross-references: EMBL:Ul1821; NID:g595430; PIDN:AAC50124.1; PID:g595431
g printed,	R.Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto,
	A; Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
	A;Reference number: JC2340; MUID:95071350 A:Accession: JC2340
or ion	A, Molecule type: DNA A: Positions: 1-281 (MTT)
i	. A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990
•	K)SCHALZIEID, C.E.
gand - rat	A) Reference number: \$57565 A) Reference number: \$57565
	A;Accession: S57565
	A. Status: preliminary
necrosis fac	A; POLECULE LYPE: MRNA A; Residues: 1-281 <sch></sch>
toxin - bovi	
necrosis tac	R;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;
necrosis fac	A; Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
necrosis fac	A; Reference number: I38554; MUID:95105731
necrosis fac	A;Accession: 138554 A;Status: Dreliminary: translated from GB/EMBL/DDBJ
e-rich prote	A; Molecule type: mRNA
necrosis fac	A;cross_references: EMBE:000137; NID:9024027; FIDN:AAC30071.1; FID:9024020 C;Genetics:
necrosis fac	A;Gene: FasL
ed surface g	A:Introns: 151/1: 116/3
n (EC 3.4.21	F;80-102/Domain: transmembrane #status predicted <tmm></tmm>
necrosis fac	F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted
necrosis tac	
n (EC 3.4.21	98.5%
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Matches

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Mismatches

0;

Indels

23;

Gaps

1;

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C;Accession: A53062

R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, Cell 76, 969-976, 1994

A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutata; Reference number: A53062; MUID:94185175

A;Accession: A53062
                                                                   C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                                                                          RESULT 3
A49266
fas ligand - rat
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A;Molecule type: mRNA
A;Residues: 1-279 <TAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Mus musculus (house mouse)
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Best Local Similarity 72.3
Matches 204; Conservative
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A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16276.1; PID:g205255 A;Note: the authors translated codon CTC for residue 172 as Ile C;Comment: This protein is structurally related pleiotropic cytokinase with C;Genetics:
A;Gene: TNF-beta
                                                                                                                                                                                                                                                                                                                               A:Introns: 32/3; 66/1
C:Superfamily: tumor necrosis factor
C:Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Cloning and sequence analysis of A;Reference number: JN0868; MUID:94040766 A;Accession: JN0869
A;Molecule type: DNA
A;Residues: 1-202 <KMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kwon, J.; Chung, I.Y.;
Gene 132, 227-236, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C;Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
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                                  PFHVPLLSAQKSVYPGLQGPWVRSMYQGAVFLLSKGDQLSTHTDGISHLHFSPSTVFFGA
                                                                                                   TDRAFLRHGFSLNNNSLLIPTSGLYFVYSQVVFSGESCSPRAIPTPIXLAHEVQLFSSQY
                                                                                                                                     TYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCN-----NLPLSHKVYMRNSKY 195
                                                                                                                                                                       LLGLLLALPLGAQGLSGVRFSASRTAHQPPQKHLTHGLLKPAAHLVGYPSKQNSLLWRAN
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                                                                                                                                                                                                                                              58;
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                                                                                                                                                                                                                                                          Score 211;
Pred. No. 1.
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-25,'p',27-202 <RES>
A; Cross-references: GB:M17015; NID:g198880; PIDN:AAA39450.1;
A; Cross-references: GB:M17015; Tang, W.L.; Ruddle, N.
                                                                                                               A;Map position: 17
A;Introns: 32/3; 66/1
C;Superfamily: tumor necrosis factor
                                                                                                    C;Superfamily: tumor
C;Keywords: cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N. Nucleic Acids Res. 15, 3937, 1987

Public: The murine tumor necrosis factor-beta (lymphotoxin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; R;Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, J. Immunol. 139, 476-483, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S10083; MUID:89144562
A;Accession: S10083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene Res. 3, 409-414, 19
A; Title: Induction of tumor
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A; Residues: 1-11;139-160, 'CG', 163-178 <NED>
A; Cross-references: EMBL: X06217
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A; Residues: 1-202 <RE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of A;Reference number: I56004; MUID:87252204
A;Accession: I56004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 6-202 <WEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including
A;Reference number: A93679; MUID:88067722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor beta precursor - moventumor necrosis factor beta precursor - moventumor necrosis factor beta
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A;Residues: 1-202 <RE2>
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A; Residues: 1-202 <SEM>
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                                                                                                                                                                                                                                                                                                                                                                                                           ;Title: Cloning and expression of murine lymphotoxin cDNA;Reference number: I55980; MUID:87224127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                 Genetics
                                                                                                                                                                                                                                                                                                                                                                                      Accession: 155980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerence number: I48853; MUID:87231097 cession: I48853
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                                                                                                    cytotoxin;
14.7%;
                                                                                                    glycoprotein; lymphokine; macrophage
Score
Pred.
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208; DB 1;
No. 1.9e-08;
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                     Length 202;
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A;Title: Cloning and structural analysis of the genes, coding for rabbit tumor necro A;Reference number: PN0098; MUID:90220566
A;Accession: PN0098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Shakhov, A.N.; Kuprash, D.V.;
Gene 95, 215-221, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor beta precursor - rabbit N; Alternate names: lymphotoxin; TNF beta
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A; Residues: 1-197 <SHA>
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A; Residues: 1-197 <SH2>
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                                                                                                                                                                                                                                                                                                                 PPGRLY-----LPLLLGLLLAPPPPGAQGLPGAEFPPSAARNAQQRLQKHFGHST----- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDRAFIRHGESLSNNSLLIPTSGLYFVYSQVVFSGESCSPRAIPTPIYLAHEVQLFSSQY 139
                                                                                          DLYMMEGKMMSYCTTGQ-MWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLY 256
                                                                                                                                   RAFLRHGFSLSNNSLLVPSSGLYFVYSQVVFSGEGCSPKAVPTPLYLAHEVQLFSSQYSF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFHVPLLSAQKSVYPGLQGPWVRSMYQGAVFLLSKGDQLSTHTDGISHLHFSPSSVFFGA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCN-----NLPLSHKVYMRNSKY 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLVALVGLGLGMFQL----FHLQKEPSPPPEKK----ELRKVAHLTGKSNSRSMPLEWED 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGLLLALPLGAQGLSGVRFSAARTAHPLPQKHLTHGILKPAAHLVGYPSKQNSLLWRAS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JH0309; PN0098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    14.5%; Score 204.5; DB 27.3%; Pred. No. 3.3e-08 tive 28; Mismatches 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Azizov, M.M.; Jongeneel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                         -LKPAAHLVGDPSAQD-SLRWRANTD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          locus, containing the genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g297168
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                                                                                                                                                                                                                                                                                                                                                                                                      55,
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C;Species: Sus scrofa domestica (domestic pig)
C;Cpate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S12606; S17290; S18955; 146659
R;Drews, R.T.; Coffee, B.W.: Practional
Nucleic and action
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A; Molecule type: mRNA
A; Residues: 1-232 < CHO>
A; Cross-references: EMBL: X57321; NID: g2137;
A; Cross-references: EMBL: X57321; NID: g2137; NID: g2137
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A; Introns: 62/3; 78/1; 93/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
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A; Residues: 44-232 <PAU>
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A; Accession: I46659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S18965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The porcine tumor necrosis factor-encoding genes: A; Reference number: S17289; MUID:91340150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S18965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: tumor necrosis factor; (Reywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myri; 1-77/Domain: propeptide #status predicted <PRO>; 78-232/Product: tumor necrosis factor alpha #status predicted <MAT>; 18, 20/Binding site: myristate (Lys) (covalent) #status predicted prinding site: carbohydrate (Ser) (covalent) #status predicted
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Best Local Similarity
Matches 68; Conserv
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        196
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                                                                                       GAVENLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 258
                                                                                                                                                                                                                                                 VYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC-----TTGQMWARSSYL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAGGPQGSRRCLCLSLFSFL--LVAGATTLFCLLHFEVIGPQKEEFPAGPLSINPLAQGL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHL-----QKE--PSPP----PEKKEL 120
        GGVFQLEKDDRLSAEINLPDYLDFAESGQVYFGIIAL 232
                                                                                                                                                                      VLFRGQGCPSTNVFLTHTISRIAVSY-QTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 195
                                                                                                                                                                                                                                                                                                                                             RSSSQTSDKPVAHVVANVKAEGQ-LQWQSGYANALLANGVKLKDNQLVVPTDGLYLIYSQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                            RK-----VAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKYKKGGLVINETGLYFVYSK 171
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A; Introns: 62/3; 78/1; 94/1
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor
C; Keywords: glycoprotein; lipoprotein; myristylation; tra
C; Keywords: glycoprotein (Lys) (covalent) #status pre
F; 20/Binding site: carbohydrate (Ser) (covalent) #status
F; 81/Binding site: carbohydrate (Ser) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor alpha precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000 C;Accession: I46047; S24642 R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L. Cytokine 5, 336-341, 1993 Cytokine 5, 336-34
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I46046; S24641
R;Cludts, T.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lympho
A;Reference number: I46046; MUID:94083525
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A; Gene: TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-233 <CL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: I46047
                                                                                                                                                                                               F;145-177/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I46046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphotoxin
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Matches
                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 LSLVNFEESQTFFGLYKL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 KSNSRSMPLEWE-DTYGIVLLSGVKYKKGGLVINETGLYFVYSKYYFRGQSC-----NN
::: | | | :| | | | :: :||||||:| | :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 PPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKEPSPPPEKKELRKVAHLTG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYLAHEVQLFSPQYPFHVPLLSAQ-KSVCPGPQGPWVRSVYQGAVFLLTRGDQLSTHTDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISHLLLSPSSVFFGAFAL 204
                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: 214137; NID: 9796; PIDN: CAA78511.1; PID: 9798
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                                     13.5%;
30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%; Score 190.5; 30.3%; Pred. No. 3.
26;
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                                     Score 190.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                    myristylation; transmembrane
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                                         . 2e-07
                                                                               DΒ
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                                                                          Length
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35;
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10;
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72 KKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHL-----

-QKEPSP----

PPEKKEL 120

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A;Cross-references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445
A;Experimental source: lymphoblastoid cell line RPMI-1788
R;Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A;Title: Tumor necrosis factors: gene structure and biological activities.
A;Reference number: A32877; MUID:87217059
A;Accession: B32877
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Molecule type: mSNA
A;Molecule type: mNA
A;Molecule type: MSNA
A;Molecule type: 
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NyAlternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta

C ples: Homo sapiens (man)

C e: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000

C; Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A01

C; Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951; A01

R; Nedwin, G.E.; Jarrett-Medwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.;

J. Cell. Biochem. 29, 171-181, 1985

A; Title: Structure and chromosomal localization of the human lymphotoxin gene.

A; Reference number: A92755; MUID: 86086150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-124, 'p', 126-205 < RES>
A; Residues: 1-124, 'p', 126-205 < RES>
A; Residues: 1-124, 'p', 126-205 < RES>
A; Residues: GB: M55913; NID: g339742; PIDN: AAB59455.1; PID: g339743
A; Note: 59-Asn was also found (ancestral haplotype 57.1
A; Note: 59-Asn was also found (ancestral haplotype 8.1)
A; Rodray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.;
Nature 312, 721-724, 1984
A; Title: Cloning and expression of cDNA for human lymphotoxin, a lymphok:
A; Reference number: A93350; MUID: 85086243
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QWHUX
A;Title: Cloning and expression of human lymphotoxin A;Reference number: A91906; MUID:87057135 A;Accession: A91906 A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S. Immunogenetics 33, 50-53, 1991
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A; Residues: 1-205 <GRA>
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A; Residues: 1-59, 'N', 61-205 < NED>
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                                                                                                                           mRNA derived
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.Y.; Goeddel,
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P
                                  Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence
A;Reference number: S17289; MUID:91340150
                                                                                                                                                                                                                                      tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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                                                                                                                       R; Kuhnert, P.; Wuethrich,
Gene 102, 171-178, 1991
                                                                                                                                                                                                        C; Accession: S17289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
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A; Cross-references: GB: D00102; NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                         C.; Peterhans,
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C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophae
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-205/Product: lymphotoxin #status predicted <MAT>
F;41/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Fukushima, K.; Watanabe, H.; Takeo, K.; Narch. Biochem. Biophys. 304, 144-153, 1993 A;Title: N-linked sugar chain structure of A;Reference number: $34742; MUID:93311995 A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after inductio while having no detrimental effect on normal cells. It can also act synergistically C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of diffical activities but are produced by different cell types and have different induction
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A; Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosyla A; Reference number: S26951; MUID: 93083656
A; Accession: S26951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:LTA; LT; TNFB
A;Cross-references: GDB:120442; OMIM:153440
A;Map position: 6p21.3-6p21.3
A;Introns: 33/3; 69/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: the first intron occurs before the initiator codon
                                                                         236 VNVSELSLVNFEESQTFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 PP--LPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKEPSPPPEKKELR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PPERLFLPRVCGTTLHLLLLGLLLVLLPGAQGLPGVGLTPSAAQTARQHPKMHLAHSTLK
                                                                                                                                                                                                                                                                                             PAAHLIGDPSKONSLLWRANTDRAFLODGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSP
THTDGIPHLVLSPSTVFFGAFAL
                                                                                                                                                  KATSSPLYLAHEVQLFSSQYPFHVPLLSSQKMVYPGLQEPWLHSMYHGAAFQLTQGDQLS
                                                                                                                                                                                                                   --SCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLY 235
                                                                                                                                                                                                                                                                                                                                                                  KVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQ---- 177
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Pred. No. 6.6e-07;
3; Mismatches 105
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A;Title: Cloning and characterization of gene A;Reference number: JQ1344; MUID:92084125
A;Accession: JQ1344
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C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-33/Domain: signal sequence #status predicted <5/50>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor alpha precursor - N; Alternate names: cachectin; TNF alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; C;Comment: This protein is an important proximal mediator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-234 <SUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: JQ1344
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                                                                                                                                                                                                                                                                                                                                                               Superfamily: tumor necrosis factor; superfamily: tumor necrosis factor; keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; keywords: cytoduct: tumor necrosis factor alpha #status predicted <TUM>;19.234/Product: tumor necrosis factor alpha #status predicted;19,20/Binding site: myristate (Lys) (covalent) #status predicted;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNF-alpha
                                                                 LRSSSRTPSDKPVAHVVANPQAEGQ-LQWLSGRANALLANGVKLTDNQLVVPLDGLYLIY 136
                                                                                                                                                    KAGGPQGSRRCLCLSLFSFL--LVAGATTLFCLLHFGVIGPQREEQLPNAFQSINPLAQT 77
                                                                                                                                                                                             KKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHL-----QKEPSPP-----PEKKE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYYMRNSKYPQDLVMMEGKMMSYCTTGQ-MWARSSYLGAVFNLTSADHLYVNVSELSLVN 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STGLCLLVMFFMVL----VALVGLGLGMFQLFHLQKEPSPPPEKKELRKVAHLTGKSNSR 133
                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                                                                          Conservative
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                                                                                                          VAHLTGKSNSRSMPLEW-EDTYGIVLLSGVKYKKGGLVINETGLYFVY 169
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                                                                                                                                                                                                                                                        12.8%; 27.9%;
                                                                                                                                                                                                                                          31;
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; Pred. No. 9.1e-07;
27; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g2132; PIDN:CAA38638.1; PID:g2133
                                                                                                                                                                                                                                        Score 181; DB 1; 1
Pred. No. 2.1e-06;
1; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-Sep-1999 #text_change
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endotoxemia
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GB: X02910;

GB:X02159;

NID: 937209;

PIDN:CAA26669.1;

PID: 937210

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tumor necrosis factor alpha precursor [validated] - human N;Alternate names: cachectin; TNFA (;Species: Homo sapiens (man) C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000 C;Accession: A93585; 35153; A93351; A44189; B61478; I53311; S62610; I54522; R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J. Nucleic Acids Res. 13, 6361-6373, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Bakalara, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M. Biochem. Biophys. Res. Commun. 166, 66-73, 1990
A;Title: Presence in invertebrate genomes of sequences characterized A;Reference number: A90159; MUID:90147742
                          A; Molecule type: mRNA
                                                  A; Reference number: A93351; A; Accession: A93351
                                                                               A; Title: Human tumour necrosis factor: precursor structure, A; Reference number: A93351; MUID:85086244
                                                                                                                               R; Pennica, D.; Nedwin, Nature 312, 724-729, 1
                                                                                                                                                    A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.;
                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-233 <IRI>
                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                           A; Accession: S36153
                                                                                                                                                                                                                                                                                                                                   A; Title: Dense Alu clustering and a potential A; Reference number: S36152; MUID: 93272029
                                                                                                                                                                                                                                                                                                                                                                                  R; Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Nature Genet. 3, 137-145, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-233 <NED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A93585; MUID:86016093 A; Accession: A93585
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A;Cross-references: GB:M32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 59-136 <
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A; Residues: 1-141 <BAK>
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  A; Residues:
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Best Local Similarity 49.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 STGLCLLVMFF 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPPPPPPPPPPPPPPPLPLPLPLPLKKRGNH 77
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                                                                                                                               724-729, 1984
1-233 <PEN>
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49.3%;
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                                                                                                                                                                                                                                                                                                                                                                new member
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                                                                                                       expression and homology
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Perrot, V:
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                                                                                                                                                                                    August 1992
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                                                                                                                                                         Palladino, M
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from a promyelc
Arsdell, J.N.;

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A;Cross-references: GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific A;Reference number: A59163; MUID:93018820
A;Reference number: A59163; MUID:93018870
A metants: annotation; identification of myristylated lysines
A;Tarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br.
J. Jol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974
A;Contents: annotation; disulfide bond
                                                                                                                       C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein;
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;D'Alfonso, S.; Richlardi, P.M. Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regic A;Reference number: I54522; MUID:94102809
A;Accession: I54522
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Eur. J. Biochem. 152, 515-522, 1985
A; tle: Molecular cloning and expression of human tumor necrosis factor and comparison a perence number: 153311; MUID:86030296
                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 62/3; C; Complex: homot
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:120441;
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction out detriment to normal cells. It can also act synergistically with interferon gamma to C;Comment: TNF-alpha and beta (lymphotoxin) are the products of different genes closely utare produced by different cell types and have different induction kinetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-8 <DAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-62, 'S',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: TNF; TNFA
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A;Experimental source: U-937 cells
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A; Residues: 1-233 <MAR>
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Query Match
Best Local Similarity
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26.8%;
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   Score 172.5; DB 1; Pred. No. 8.6e-06;
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A;Residues: 1-389 <SAZ>
A;Cross-references: GB:D10727; NID:g220499; PIDN:BAA01570.1; PID:d1002045;
                                                                                                                                                                                                                                                                      A;Reference number: S27200; MUID:93041923
A;Accession: S27200
                                                                                                                                                                                                                                                                                                                                 R; Sazuka,
                                                                                                                                                                                                                                                                                                                                                   C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S27200
                                                                                                                                                                                                                                                                                                                                                                                   proline-rich protein - mouse
C; Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                       Query Match
Best Local Similarity
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                                                                               SPWAPPGTV---LPCPTSVPRRPGQRRPPPPPPPPPPPPPPPPPPPLPPLPPLKKRGNHS
                               TGLCLLVMFFMVLVALVGLGLGMFQLFHLQKEPSPPP 115
                                                           SPTAPNGSLDSVTYPVSPPPTSGPAAPPPPPPP---PPPPPPPPPPPPPPLPPLA-----
                                                                                                                                                                                                                                                                                                                                     T.; Tomooka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVRSSSRTPSDK----PVAHVVANPQAEGQ-LQWLNRRANALLANGVELRDNQLVVPSEG 130
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-SLSHCGSQASPPP
                                                                                                                                          Score 172.5; DB 2
Pred. No. 1.5e-05;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on:
April 24, 2001, 15:33:06; Search time 26.96 Seconds (without alignments) 706.092 Million cell updates/sec Title:
Sequence:
1504
Sequence:
1504
Sequence:
1 MQOPFNYPYPQIYWYDSSAS......SELSIVNFEESQTFFGLYKL 277
Scoring table:
Gapop 10.0; Gapext 0.5
Searched:
198801 seqs, 68722935 residues
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Ch Ch		DB 2	ID 138707	Description Fas ligand - human
) N	1127	74.9	279	N	A53062	ligand -
з	1107.5		278	ນ	A49266	ligand -
4	208	13	202	Ц	в27303	or necrosi
ر. ت	208	13	202	Н	JN0869	necrosis
6	195	13	197	Н	JH0309	tumor necrosis fac
7	194	12	205	\vdash	X UHMÖ	otoxin alp
8	187.5	12	232	Н	S12606	tumor necrosis fac
9	185.5		204	<u>, , , , , , , , , , , , , , , , , , , </u>	S17289	necrosis
10	185.5	12	234	Н	JQ1344	
11	182.5	12.1	204	ب	S24641	otoxin - k
12	182	12.1	233	Н	S24642	
13	177	11.8	141	N	A34043	hypothetical proli
14	176		233	Н	NUHWÖ	tumor necrosis fac
15	174		233	Н	S22052	tumor necrosis fac
16	173	11.5	234	Н	A25451	tumor necrosis fac
17	172	11.4	599	N	T10798	pherophorin-S - Vo
18	171.5	11.4	415	ᆫ	A34170	acrosin (EC 3.4.21
19	169.5	11.3	185	N	S52715	tumor necrosis fac
20	169.5	11.3	485	N	A33647	sulfated surface g
21	165.5	11.0	389	2	S27200	proline-rich prote
22	164		235	Ν	I54490	tumor necrosis fac
23	163.5	10.9	306	N	149139	lymphotoxin-beta -
24	163	10.8	233	N	S11688	tumor necrosis fac
25	163	10.8	431	ν	S47538	
26	162.5	10.8	234	_	JH0529	tumor necrosis fac
27	161	10.7	193	N	S06192	
28	160.5	10.7	1206	v	524407	
၁	100			ŧ	104470	AT MITOTOST MINITOT

Query Match 99.2%; Score 1492; DB 2; Length 281; Best Local Similarity 98.6%; Pred. No. 5.3e-103; Matches 277; Conservative 0; Mismatches 0; Indels

4;

Gaps

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45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30
148	149.5	150	150.5	150.5	151	151	151	152	153	154.5	154.5	155	155.5	159	159.5
9.8	9.9	10.0	10.0	10.0	10.0	10.0	10.0	10.1	10.2	10.3	10.3	10.3	10.3	10.6	10.6
1171	645	1460	1255	464	980	439	196	487	760	1110	502	235	440	235	421
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T17454	A71416	EDBEIF	T31065	S22697	S54986	S51939	B48232	S42442	T06291	T19673	A55197	JU0029	149681	OWMSN	S11674
diaphanous-related	hypothetical prote	immediate-early pr	diaphanous protein	extensin - Volvox	regulatory protein	chitinase (EC 3.2.	cysteine-rich exte	nuclear protein EB	extensin homolog T	hypothetical prote	Wiskott-Aldrich sy	tumor necrosis fac	glyceraldehyde-3-p	tumor necrosis fac	acrosin (EC 3.4.21

ALIGNMENTS

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A; Accession: 138554 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-281 <re2> A; Residues: 1-281 <re2> A; Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628 C; Genetics: C; Genetics: A; Gene: FasL A; Introns: 151/1; 116/3 C; Keywords: glycoprotein; transmembrane protein F; 80-102/Domain: transmembrane #status predicted <tmm> F; 76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted</tmm></re2></re2>	A;Accession: JC2340 A;Accession: JC2340 A;Molecule type: DNA A;Residues: 1-281 (ANIT> A;Residues: 1-281 (ANIT> A;Residues: 1-281 EMBL Data Library, June 1995 A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990 R;Cchatzlein, C.E. Submitted to the EMBL Data Library, June 1995 A;Reference number: S57565 A;Reference number: S57565 A;Reference number: MRNA A;Residues: 1-281 (SCH> A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456 A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456 A;Cross-references: EMBL:X89102; NID:g887455; PID:g887456 A;Title: Fast ligand mediates activation-induced cell death in human T lymphocytes. A;Reference number: I38554; MUID:95105731	RESULT 1 138707 Fas ligand - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000 C;Accession: 138707; JC2340; S57565; 138554 R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S. Int. Immunol. 6, 1567-1574, 1994 A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici A;Reference number: 138707; MUID:95127560 A;Accession: 138707 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues; 1-281 <res> A;Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431 R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Biophys. Res. Commun. 204, 468-474, 1994 A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection. A;Reference number: JC2340; MUID:95071350</res>

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rs 37052

A537052

Fas ligand - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #sequence_re
     fas ligand - rat
C;Specles: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1996
C;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata,
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the
A;Reference number: A49266; MUID:94084792
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                                                                                                                                                                                                                                                                                                        AHSSYLGAVFNLTSADHLYVNISQLSLINFEESKTFFGLYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHTASSLEKQIGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGG
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214; Conserv
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Pred. No. 4.1e-76;
6; Mismatches 34;
                                                                                                                              13-Jan-1995 #text_change
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                                of
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                                the tumor
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C;Keywords: glycoprotein; transmembrane protein
       A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-25.'P',27-202 <RES>A;Cross-references: GB:M17015; NII
                                                                                                                                                                                                                                                                                                                         Oncogene Res. 3, 409-414, 1988
A; Title: Induction of tumor necrosis factor-alpha
A; Reference number: S10083; MUID:89144562
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                                                                                                                            A; Title: Mouse lymphotoxin and tumor necrosis A; Reference number: 156004; MUID:87252204
                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 6-202 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-11; 139-160, 'CG', 163-178
A; Cross-references: EMBL: X06217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-202 <SEM>
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                                                                                                     A; Accession: I56004
                                                                                                                                                                                                                                                                                                   A; Accession: S10083
                                                                                                                                                                                                                                                                                                                                                                                                   R; Weil, D.; Dautry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 73.1
Best Local Similarity 75.3
Matches 212; Conservative
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75.2%; Pred. No. 1.1e-74;
Live 22; Mismatches 39
<RES>
15; NID:g198880;
                                                                                 from GB/EMBL/DDBJ
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          PIDN: AAA39450.1;
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clon

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A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68529.1; PID:g54831 R;Nedospasov, S.A.; Hirt, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, nucleic Acids Res. 14, 7713-7725, 1986 A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxia, Reference number: S01342; MUID:87040736 A;Accession: S01342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NyAlternate names: lymphotoxin; TNF beta
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: B27303; S01342; S10083; I56004; I48853; I55980
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alph
A;Reference number: A93679; MUID:88067722
                                                                                                                                                                                         A;Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269 R;Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D. J. Immunol. 139, 476-483, 1987
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                                                                                                                                                                    Structural analysis
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PID: 9387407
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                                                                                                                                                                       of the
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Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of A;Reference number: JN0868; MUID:94040766
A;Accession: JN0869
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                   Š
                                                                                                                                                                                          A; Gene: TNF-beta
A; Introns: 32/3;
                                                                                                                                                                                                                                  C;Comment: This protein
C;Genetics:
                                                                                                                                                                                                                                            A;Cross-references: GB:L00981; NID:g205253; PIDN:AAA16276.1; PID:g205255 A;Note: the authors translated codon CTC for residue 172 as Ile C;Comment: This protein is structurally related pleiotropic cytokinase with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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A; Residues: 1-202 <RE2>
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A;Title: The murine tumor necrosis factor-beta (lymphotoxin) A;Reference number: I48853; MUID:87231097
A;Accession: I48853
                                                                                                                                                                                                                                                                                                          A; Residues: 1-202 < KWO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-202 < RE3>
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                                                                                                                                                         Superfamily: tumor
Keywords: tumor
                                                                                                                                                                                                                                                                                                                                                                                                       Kwon, J.; Chung, I.Y.; Benveniste, ene 132, 227-236, 1993
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Best Local
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e: 10
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cies: Rattus norvegicus (Norway
160
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                                                                           Local
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mes 52; Conservative
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                                                         Similarity
54; Conserv
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                                                   Score 208; DB 1; Lei
Pred. No. 1.5e-08;
"" matches 71;
                                                         28;
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Pred. No. 1.5e-08;
Pred. No. 1.5e-08;
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on 10-sep-1999
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5'-untranslated
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                                                                                             Length 202
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C.Accession: A92755; S36154; I54482; A93350; B32877; A91906; A61478; S26951;
C.Accession: G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit
A;Reference number: JH0309; MUID:91065534
                     R; Nedwin, G.E.; Jarrett-Nedwin, J.;
J. Cell. Biochem. 29, 171-181, 1985
                                                                                                                                           lymphotoxin alpha precursor - human N; Alternate names: lymphotoxin A; T
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C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine;
F;1-26/Domain: signal sequence #status predicted <SIG>
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A;Title: Cloning and Structural analysis of the genes, coding for rabbit tumor necros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-197 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: PN0098; MUID:90220566
A;Accession: PN0098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N; Alternate names: lymphotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor beta precursor -
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A; Residues: 1-197 <SH2>
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                                                                                                                                                                                                                                                                                                                                                                                                                       KGGLVINETGLYFVYSKVYFRGQSCN-----NLPLSHKVYMRNSKYPQDLVMMEGKMMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NAQQRLQKHFGHST-----LKPAAHLVGDPSAQD-SLRWRANTDRAFLRHGFSLS
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                                                                                                                                                                                                                                                                                VCPGPQGPWVRSVYQGAVFLLTQGDQLSTHTDGIAHLLLSPSSVFFGAFAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
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                                                                                                                                         lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 195; DB 1;
Pred. No. 1.3e-07;
7; Mismatches 84
localization of the human lymphotoxin
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                                             Sakaguchi, A.Y.;
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                                                                        A01645;
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A; Nolecule type: protein
A; Nolecule type: protein
A; Residues: 35-59,'N',61-205 <VOI>
A; Residues: 35-59,'N',61-205 <VOI>
A; Note: 60-Thr.was also found
R; Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, Arch. Biochem. Biophys. 304, 144-153, 1993
A; Title: N-linked sugar chain structure of recombinant human
A; Reference number: S34742; MUID:93311995
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A;Experimental source: lymphoblastoid cell line RPMI-1788
R;Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A;Title: Tumor necrosis factors: gene structure and biological activities.
A;Reference number: A32877; MUID:87217059
A;Accession: B32877
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Natural human tumor necrosis factor A; Reference number: S26951; MUID:93083656
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A;Residues: 56-79;86-95,'X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',
R;Voigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
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A;Title: Cloning and expression of cDNA for A;Reference number: A93350; MUID:85086243
A;Accession: A93350
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                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S26951
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Sidues: 1-59, 'N', G81-205 < KOB>
Solues: 1-59, 'N', G81-205 < KOB>
Solues: 1-59, 'N', G81-205; NID:g219913; PIDN:BAA00064.1; PID:g219914
A; Mote: the authors translated the codon TAT for residue 156 as Thr and ACC for R; Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, Lymphokine Res. 7, 175-185, 1988
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Immunogenetics 33, 50-53, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S36154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature Genet.
                                                       Comment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Simultaneous production of natural Reference number: A61478; MUID:88301617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: I54482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.;
ture Genet. 3, 137-145, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tus: translation not shown; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dues: 1-124,'P',126-205 <RES>
                                                   Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -59,'N',61-205 <NED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequence not shown;
                                               from mitogen-activated lymphocytes
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           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human lymphotoxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta (lymphotoxin). Variable O-glycosylati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
               cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor-alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                               within 1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not
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           can also
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                                                                                                                                                                                                                                             T.;
                                                                                                                                                                  lymphotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a lymphokine with tumour
days after induction act synergistically
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                                               after induction,
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K.I.; An
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               ¥i.ti
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                                                                                                                                                                                                                                                                                                                                                                                        A;Note: the authors translated the codon GAG for r R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a c
                                               R;Pauli, U.; Beutler, B.; Peterhans, Ē. Gene 81, 185-191, 1999.
A;Title: Porcine tumor necrosis factor alpha: A;Reference number: I46659; MUID:90034181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The porcine tumor necrosis factor-encoding genes: stage of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X54001; NID:g2135; R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Gene 102, 171-178, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-232 < DRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; Nucleic Acids Res. 18, 5564, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ωy
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A; Introns: 33/3; 69/1
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                                                                                                                                                              A;Cross-references: EMBL:X57321; NID:g2137; R;Pauli, U.; Beutler, B.; Peterhans, E.
                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-232 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: S12606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Gene sequence of porcine tumor necrosis A; Reference number: S12606; MUID: 91016861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
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                                                                                                                                                                                                                                                                                                                    A; Accession: $18965
                                                                                                                                                                                                                                                                                                                                                    A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S12606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e tumor necrosis factor-encoding genes: sequence and comparative {\tt S17289;\ MUID:91340150}
                                                                                                                                                                                                                                                                                                                                                            S18965
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PIDN:CAA40591.1;

PID: g2138

residue CDNA

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encoding

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tumor

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Cloning

with

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polymerase

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PIDN:CAA37949.1; Pauli, U.

PID:g2136

factor alpha

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tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S12606; S17290; S18965; I46659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: the first intron occurs before the initiator codon C; Superfamily: tumor necrosis factor C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; F; 1-34/Domain: signal sequence #status predicted <SIG>F; 1-34/Domain: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;41/Binding site: carbohydrate (Thr) (covalent) (partial) #status ex F;96/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;35-205/Product: lymphotoxin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 YVNVSELSLVNFEESQTFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 LCLLVMFFMVLVALVGL-GLGMFQLFHLQKELAELRESTSQMHTASSLGHPSPPPEKKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLLGLLLVLLPGAQGLPGVG------LTPSAAQTARQHPKMHLAHST-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STHTDGIPHLVLSPSTVFFGAFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SCNNLPLSHKVYMRNSKYPODLVMMEGKMMSYCTTGOMWARSSYLGAVFNLTSADHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKATSSPLYLAHEVQLFSSQYPFHVPLLSSQKMVYPGLQEPWLHSMYHGAAFQLTQGDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein and TNF-alpha (tumor necrosis factor) are the products of diff but are produced by different cell types and have different induction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDB:120442; OMIM:153440
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27.5%;
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Pred. No. 1.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                         04 - Feb - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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C;Superfamily: tumor necrosis factor C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymp F;1-77/Domain: propeptide #status predicted F;1-77/Product: tumor necrosis factor alpha #status predicted F;19,20/Binding site: myristate (Lys) (covalent) #status predict F;81/Binding site: carbohydrate (Ser) (covalent) #status predict F;144-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor beta precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
                                                                         В
                                                                                                                  δÃ
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                               ρy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 102, 171-178, 1991
A; Title: The porcine tumor r
A; Reference number: S17289;
A; Accession: S17289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kuhnert,
                                                                                                                                                                                                                                                                                                                                       ;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;1-33/Domain: signal sequence #status predicted <SIG>;34-204/Product: tumor necrosis factor beta #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Accession: S17289
;Kuhnert, P.; Wuet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Genetics:
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oss-references: EMBL:X54859; NID:g2132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ecule type: DNA
idues: 1-204 <KUH>
112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , P.; Wuethrich,
171-178, 1991
                                   VYFRGQSC-----NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQ-MWARSSYLGA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPEGAEAKPWYEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFGIIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQLVVPTDGLYLIYSQVLFRGQGCPSTNVFLTHTISRIAVSY-QTKVNLLSAIKSPCQRE 179
                                                                         KHLARGTLKPAAHLVGDPSTPD-SLRWRANTDRAFLRHGFLLSNNSLLVPTSGLYFVYSQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGLVINETGLYFVYSKVYFRGQSC -- NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC -- -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTSQMHTASSLGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKYKK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAGGPQGSRRCLCLSLFSFL--LVAGATTLFCLLHFEVIGPQKEEFPAGPLSINPLAQGL 77
VVFSGEGCFPKATPTPLYLAHEVQLFSSQYPFHVPLLSAQ-KSVCPGPQGPWVRSVYQGA
                                                                                                                  PE--KKELRKVAHLTGKSNSRSMPLEWE-DTYGIVLLSGVKYKKGGLVINETGLYFVYSK 190
                                                                                                                                                                                                  STGLCLLVMFFMVL----VALVGLGLGMFQLFHLQKELAELRESTSQMHTASSLGHPSPP 133
                                                                                                                                                            STPILLLEGLLLALPPEAQGLPGVGL---
                                                                                                                                                                                                                                          62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 29.2
68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         tumor necrosis factor
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                                                                                                                                                                                                                                                           12.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                necrosis factor-encoding; MUID:91340150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---KPVAHVVANVKAEGQ-LQWQSGYANALLANGVKLKD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 187.5; DB 1; Pred. No. 5.7e-07;
                                                                                                                                                                                                                                          Score 185.5; DB 1;
Pred. No. 6.9e-07;
B; Mismatches 87;
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                                                                                                                                                        ------PPSAAQPAHQHPP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes:
                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g2133
                                                                                                                                                                                                                                                                                  204;
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              A; Introns: 32/3; C; Superfamily: tu
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C;Date: 10-569 437, S24641
C;Accession: T46046, S24641
R;Cludts, I; Cleuter, Y.; Kettmann, R.; Burn:
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the
                                                                                                                                                                                                                                                                         lymphotoxin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage;
E;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;846-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 191
A;Title: Cloning and characterization of gene TNF
A;Reference number: JQ1344; MUID:92084125
                                                                                                                                     A; Reference number: I46046; A; Accession: I46046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; C;Comment: This protein is an important proximal mediator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-234 <SUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Equus caballus (domestic ho)
C;Date: 10-Sep-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor alpha precursor - N;Alternate names: cachectin; TNF alpha
                                          A; Cross-references:
                                                                  A; Molecule type: DNA A; Residues: 1-204 <C
                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: TNF-alpha
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                   Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 LYLIYSQVLFKGQGCPSTHVLLTHTISRLAVSYPSKVNLLSA-IKSPCHTESPEQAEAKP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         WYEPIYLGGVFQLEKGDQLSAEINQPNYLDFAESGQVYFGIIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYFVYSKVYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTT------GQM 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSLGHPSPPPEKKELRKVAHLTGKSNSRSMPLEW-EDTYGIVLLSGVKYKKGGLVINETG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAGGPQGSRRCLCLSLESFL--LVAGATTLFCLLHFGVIGPQREEQLPNAFQSINPL--A 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Conserv
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68/1
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                                            EMBL: Z14137;
                                                                                                                                                                                                                                 .; Kettmann, R.; Burny,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%;
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                                          NID: 9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 185.5; DB 1
Pred. No. 8.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-Sep-1999 #text_change
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                                            PIDN:CAA78510.1;
                                                                                                                                                                                     tandemly arranged
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                                          PID:9797
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endotoxemia
                                                                                                                                                                                       bovine
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tumor

necrosis

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C; Specie
C; Date:
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C;Superfamily: tumor necrosis factor
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; tra
F;20/Binding site: myristate (Lys) (covalent) #status pre
F;81/Binding site: carbohydrate (Ser) (covalent) #status
F;145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor necrosis factor alpha precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000 C;Accession: I46047; S24642 R;Cludts, I; Cleuter, Y; Kettmann, R.; Burny, A.; Droogmans, L. Cytokine 5, 336-341, 1993 Cytokine 5, 336-341, 1
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A; Accession: 146047
A; Accession: 146047
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A; Gene: TNFA
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A; Residues: 1-233 <CL2>
A; Cross-references: EMB
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hypothetical proline-rich protein 1 - polychaete (Owenia C;Species: Owenia fusiformis C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 KKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHL-----QKE------LAELR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 LVGLGLGMFQLFHLQKELAELRESTSQMHTASSLGHPSPPP-EKKELRKVAHLTGKSNSR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                       NQLVVPADGLYLIYSQVLFRGQGCPSTPLFLTHTISRIAVSY-QTKVNILSAIKSPCHRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGLVINETGLY FVYSKVYFRGQSCNNLP--LSHKVYMRNSKYPQDLVMMEGKMMSYC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESTSOMHTASSLGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKYKK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEESQTFFGLYKL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVYMRNSKYPQDLVMMEGKMMSYCTTGQ-MWARSSYLGAVFNLTSADHLYVNVSELSLVN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-SLRWRANTDRAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGRGCFPRATPTPLYLAH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMPLEWE-DIYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSC-----NNLPLSH 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLLGL----LLALPLEAQGLRGIGLTPSAAQPAHQQLPTPFTRGTLKPAAHLVGDPSTQ 73
                                                                                                                                                                                                                                                                                                                                                      ----TTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAGGPQGSRSCLCLSLFSFL--LVAGATTLFCLLHFGVIGPQREESPGGPSINSPLVQTL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVQLFSPQYPFHVPLLSAQ-KSVCPGPQGPWVRSVYQGAVFLLTRGDQLSTHTDGISHLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NKPVAHVVADINSPGQ-LRWWDSYANALMANGVKLED 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
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Pred. No. 1.2e-06;
5: Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 182; DB 1;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
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                                                                                    fusiformis) (fragment)
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        01-Dec-2000
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A;Residues: 1-233 <IRI>
A;Residues: 1-233 <IRI>
A;Cross-references: EMBL:215026; NID:937211; PIDN:CAA78745.1; PID:937212
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
A:Pennica. D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names: cachectin;
C; Species: Homo sapiens (man)
C; Date: 28-Aug-1985 #sequence
C; Accession: A93585; S36153;
                  R; Fukuda, S.; Ando, S.; Sanou, o
Lymphokine Res. 7, 175-185, 1988
                                                                                                                                                                                                                                                            A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; P:A;Note: this protein was isolated from the monocyte-like cell line HL-60 R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Science 228, 149-154, 1985
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A:Title: Presence in invertebrate genomes of sequences characterized A:Reference number: A90159; MUID:90147742
                                                       A;Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198 R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.;
                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-62,'S',64-233 <WAN>
                                                                                                                                                                                                     A; Title: Molecular cloning of the complementary A; Reference number: A44189; MUID:85142190
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-233 <PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A93351; A; Accession: A93351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Human tumour necrosis factor: precursor structure, expression A; Reference number: A93351; MUID:85086244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Pennica, D.; Nedwin, G.
Nature 312, 724-729, 1984
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A;Accession: S36153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Iris, F.J.M.; Bougueleret, L
Nature Genet. 3, 137-145, 1993
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A; Residues: 1-233 <NED>
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A; Residues: 1-141 <BAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Human lymphotoxin and tumor necrosis
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A; Residues: 59-136 <BA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor alpha precursor [validated] -
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Best Local S
Matches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASSPWAPPGTVLPCPTSVPRRPGQRRPPPPPPPPPPPPPPPPPPPPPLPPLPPLKKRGNH
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production of natural
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49.3%;
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Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
   human
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necrosis factor-alpha,
                                                          .1; PID:g339738
Masaki, N.; Na
                                                             N.; Nakamura,
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                                                             K. I.;
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A;Reference number: A614/8; Mulling A;Accession: B61478
A;Accession: B61478
A;Accession: B61478
A;Accession: B61478
A;Residues: B3-102:109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
A;Residues: B3-102:109-119;121-128,'X',146,'XXX',150-152;159-174;180
A;Residues: B3-102:109-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-119;121-128,'X',140-1
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A.Title: A polymorphic variation in a putative regulation box A.Reference number: I54522; MUID:94102809
A.Accession: I54522
A.Status: -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Molecular cloning
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A;Title: Human tumor necrosis factor. Production, purification, A;Reference number: A92511; MUID:85130974
A;Contents: annotation; disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Myristyl acylation of the tumor necrosis factor alpha A;Reference number: A59163; MUID:93018820
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A;Experimental source: U-937 cells
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A; Residues: 1-233 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Stevenson, F.T.; Bursten, S.L.;
J. Exp. Med. 176, 1053-1062, 1992
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A; Residues: 1-8 <DAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: O-Glycosylated species of natural Reference number: S62610; MUID:96202967 Accession: S62610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: tumor necrosis factor; Reywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; Reywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; l-76/Domain: propeptide #status predicted <PRO>;77-233/Product: tumor necrosis factor #status experimental <MAT>;19.20/Binding site: myristate (Lys) (covalent) #status experimental; 19.20/Binding site: carbohydrate (Ser) (covalent) (partial) #status ex;145-177/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Status: translated from GB/EMBL/DDBJ
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GDB:120441; position: 6p21.3-6p21.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of detriment to normal cells. It can also act synergistically with interferon gonement: TNF-alpha and -beta (lymphotoxin) are the products of different genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:S68530; NID:g544751
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D'Alfonso, S.; Richiardi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are produced by different cell types and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mplex: homotrimer
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J. Biochem. 235, 431-437, 1996
                                                                                                                                                                                          114 LRESTSQMHTASSLGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKY 172
                                                                                                                     76
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                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
PLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHL----QKE------LAE 113
                                                                                                                                                                                                                                                                      PKKTGGPQGSRRCLFLSLFSFLI--VAGATTLFCLLHFGVIGPQREEFPRDLSLISPLAQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%;
27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 176; DB 1
Pred. No. 4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                             -VAHVVANPQAEGQ-LQWLNRRANALLANGVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 233
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                46;
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submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-233 <SAN>
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;145-177/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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Best Local S
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179
                                         230
                                                                                                                         173 KKGGLVINETGLYFVYSKVYFRGQSC--NNLPLSHKVYMRNSKYPQDLVMMEGKMMSYC- 229
                                                                                                                                                                                                                                                             18
                                                                                                                                                                      76 AVRSSSRT-----PSDKP-----VAHVVANPQAEGQ-LQWLNRRANALLANGVEL 119
                                                                                                                                                                                                                                                                                                  70 PLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHL-----QKE------LAE 113
                                                                                                                                                                                                               LRESTSQMHTASSLGHPSPPPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLL-SGVKY 172
                                                                                                                                                                                                                                                           PKKTGGPQGSRRCLFLSLFSFL--LVAGATTLFCLLHFGVIGPQREEFPKDPSLISPLAQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTHTISRIAVSY-QTKVNLLSAIKSPCQ 178
RETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233
                                      ----TTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEES-QTFFGLYKL 277
                                                                                  RDNQLVVPSEGLYLIYSQVLFKGQGCPSTHVLLTHTISRIAVSY-QTKVNLLSAIKSPCQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S22052
                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                    11.6%;
                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                             Score 174; DB
Pred. No. 5.7e
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 baboon
                                                                                                                                                                                                                                                                                                                                                                    DB 1;
.7e-06;
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Database: Issued_Patents_N/Database sequences: 302621
Database length: 87301344
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-996-139-12 + 185.00 256.39

_6/ptodata/2/ina/6B_COMB.seq:US-07-705-490-1 - 180.00 235.55

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_6/ptodata/2/ina/6B_COMB.seq:US-07-751-891B-1 + 178.50 250.67

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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-855-825-11 + 237.50 335.15 4 4e-11  
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-670-354-5 + 187.00 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Apr 28,
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'cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-810-453-1 + 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_p2n.model -DEV=x1p
-Q=/cgn2_1/USPTO_spool/US9508849/runat_24042001_153530_23687/app_query.fasta_1.655
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-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
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-MATRIX-blosum62 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200
-THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -MAXLEN=200000000
-QTEMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=2000000000
-R-US9508849_@CGN1_1_67 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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                                                                     /ptodata/2/ina/5B_COMB.seq:US-08-889-909A-1 + 172.50

/ptodata/2/ina/6B_COMB.seq:US-09-165-264-11 - 172.00

/ptodata/2/ina/6B_COMB.seq:US-09-165-264-13 - 171.00

/ptodata/2/ina/6B_COMB.seq:US-09-165-264-7 - 170.00

/ptodata/2/ina/6B_COMB.seq:US-09-165-264-7 - 170.00

/ptodata/2/ina/6B_COMB.seq:US-09-165-264-12 - 165.00
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256.90 1.0e-06
35.55 1.6e-05
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-452-872-1
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Patent No. (
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17 rSerAlaSerSerProTrpAlaProProGlyThrValLeuProCysProT
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                                                                                                                 MetGlnGlnProPheAsnTyrProTyrProGlnIleTyrTrpValAspSe 17
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US-09-508-849-1 x US-08-815-190A-1
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; OTHER INFORMATION:
US-08-815-190A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-815-190A-1
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Align seg 1/1 to: US-08-815-190A-1 from: 1
                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
COMPUTER: IF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                      Quality: 1389.50
Ratio: 5.386
milarity: 91.815
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SYSTEM: PC-DOS/MS-DOS
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                                                                                      Gaps: 1
Percent Identity: 91.815
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                                                              Sequence 1, Application US/08810453
Patent No. 5858990
GENERAL INFORMATION:
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT
TITLE OF INVENTION: PROLIFERATIVE DISORDERS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                   244 lAsnPheGluGluSerGlnThrPhePheGlyLeuTyrLysLeu 258
                                                                                                                                                                                                                                                                                                 701
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                                                                                                                                                                                                                                                                                              GGCAAGTCCAACTCAAGGTCCATGCCTCTGGAATGGGAAGACACCTATGG
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                                                                                                                                                                           CAATTTTGAGGAATCTCAGACGTTTTTCGGCTTATATAAGCTC 843
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alignment_block:
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US-08-810-453-1
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                                                                                                                                                                                    US-09-508-849-1 x US-08-810-453-1
                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
FEATURE:
NAME/KEY:
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LOCATION:
FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 02210-2211
COMPUTER READABLE FORM:
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1790 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: S1
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (617)720-3500
TELEFAX: (617)720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic
                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                  86
NAME/KEY:
LOCATION:
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                           Quality: 1389.50
Ratio: 5.386
milarity: 91.815
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86..931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       "transmembrane domain, amino acids 81-102" 326..391
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seq_documentation_block:
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                                                                                                                                                                          Sequence 1, Application PC/TUS9500362 GENERAL INFORMATION:
         STREET: 51 ULL...
STREET: Seattle
CITY: Seattle
STATE: WA
TOTATRY: US
                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporati
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IMMUNEX CORPORATION TITLE OF INVENTION: Ligand That Binds NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                           244 lAsnPheGluGluSerGlnThrPhePheGlyLeuTyrLysLeu 258
                                                                                                                                                                                                                                                                                                                                                                836
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COUNTRY: US
ZIP: 98101
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                                                                                       Immunex Corporation
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alignment_scores:
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PCT-US95-00362-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1841 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 01-FEB-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Maintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
                                   393
                                                                                                                                                                       293
                                                                                                                                                                                                                                         243 CCGCCACCACTACCACCTCCGCCGCCGCCGCCACCACTGCCTCCACTACC
                                                                                                                                                                                                                                                                                                          193 CCTCTGTGCCCAGAAGGCCTGGTCAAAGGAGGCCACCACCACCACCGCCA
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                                                                                                                     84 euValMetPhePheMetValLeuValAlaLeuValGlyLeuGlyLeuGly 100
                                                                                                                                                                                       67 oLeuProProLeuLysLysArgGlyAsnHisSerThrGlyLeuCysLeuL
                                                                                                                                                                                                                                                         51 ProProProLeuProProProProProProProLeuProLeuPr
                                                                                                                                                                                                                                                                                                                          34 hrSerValProArgArgProGlyGlnArgArgProProProProProPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 ATGCAGCAGCCCTTCAATTACCCCATATCCCCAGATCTACTGGGTGGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/
FILING DATE: 06-JAN-1995
                                                              MetPheGlnLeuPheHisLeuGlnLysGlu.......
                                                                                                                                                                       GCTGCCACCCCTGAAGAAGAGAGGGAACCACAGCACAGGCCTGTGTCTCC
                                TTGTGATGTTTTTCATGGTTCTGGTTGCCTTGGTAGGATTGGGCCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1389.50
Ratio: 5.386
milarity: 91.815
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Percent Identity:
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443 TACCAGCCAGATGCACACAGCATCATCTTTGGAGAAGCAAATAGGCCACC

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APPLICANT: Dean, Nicholas M.
APPLICANT: MATCUSSON, Eric G.
TITLE OF INVENTION: Antisense Compound modulation of
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
DBER OF SEQ ID NOS: 85
TWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
; Sequence 24, Applicati
                                                alignment_scores:
   Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                DATABASE ACCESSION NUMBER: D31822/Genbank DATABASE ENTRY DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6204055
                                                                                                                                                                                         PUBLICATION: (189)..(1034)
PUBLICATION INFORMATION:
JOURNAL: Biochim. Biophys. Acta
YOLUME: 204
TECHNOLOGY
                                                                                                                                                 ISSUE: 2
PAGES: 468-474
DATE: 1994-10-28
                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STyrProGlnAspLeuValMetMetGluGlyLysMetMetSerTyrCysT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    snGluThrGlyLeuTyrPheValTyrSerLysValTyrPheArgGlyGln 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yIleValLeuLeuSerGlyValLysTyrLysLysGlyGlyLeuVallleA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roSerProProProGluLysLysGluLeuArgLysValAlaHisLeuThr
   Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerCysAsnAsnLeuProLeuSerHisLysValTyrMetArgAsnSerLy 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTGTCCTGCTTTCTGGAGTGAAGTATAAGAAGGGTGGCCTTGTGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATTTTGAGGAATCTCAGACGTTTTTCGGCTTATATAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuThrSerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeuVa 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTATCCCCAGGATCTGGTGATGATGGAGGGGAAGATGATGAGCTACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTGCAACAACCTGCCCCTGAGCCACAAGGTCTACATGAGGAACTCTAA 742
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Quality: 1389.50
Ratio: 5.386
milarity: 91.815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/09290640
 Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq:US-09-290-640-24
                                Length:
 91.815
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alignment_block:
US-09-508-849-1 x US-09-290-640-24
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          244
                                                   228
                                                                                  211 hrThrGlyGlnMetTrpAlaArgSerSerTyrLeuGlyAlaValPheAsn
                                                                                                                                    194
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                                                                                                                                                                                              lAsnPheGluGluSerGlnThrPhePheGlyLeuTyrLysLeu
                                                                                                                            sTyrProGlnAspLeuValMetMetGluGlyLysMetMetSerTyrCysT
                                                                                                                                                       yIleValLeuLeuSerGlyValLysTyrLysLysGlyGlyLeuValIleA
                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuThrSerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeuVa
                                                                        CTACTGGGCAGATGTGGGGCCCGCAGCAGCTACCTGGGGGCAGTGTTCAAT
                                                                                                                GTATCCCCAGGATCTGGTGATGATGAGGGGAAGATGATGAGCTACTGCA
                                                                                                                                                                                                                                                                                                                         CCAGTCCACCCCCTGAAAAAAAGGAGCTGAGGAAAGTGGCCCATTTAACA
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CAATTTTGAGGAATCTCAGACGTTTTTCGGCTTATATAAGCTC

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-00362-4

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alignment_block:
US-09-508-849-1 x PCT-US95-00362-4
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                                                                                                                                                                                                                                                         Align seg 1/1 to: PCT-US95-00362-4 from: 1 to: 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/179,138

FILING DATE: 07-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,559

FILING DATE: 01-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: ANDESSON, KALTYON A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 32,05-WO

INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00362
FILING DATE: 06-JAN-1995
CLASSIETT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
S95-00362-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: Ligand That Binds Fas Antigen
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1171 base pairs
                                  131 CTTGTGGGCCTAGAGGGCCGGACCAAAGGAGACCGCCACCTCCACCACCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                         34 hrSerValProArgArgProGlyGlnArgArgProProProProProProPro 50 ::
51 ProProProLeuProProProProProProProProLeuProProLeuPr 67
                                                                                                          81 CAGTGCCACTTCATCTTGGGCTCCTCCAGGGTCAGTTTTTCCCTGTCCAT 130
                                                                                                                             17 rSerAlaSerSerProTrpAlaProProGlyThrValLeuProCysProT 34
                                                                                                                                                                             STREET: 51 Uni
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ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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51 University Street
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31..870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                          Length: 281
Gaps: 3
Percent Identity: 71.174
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	; ZIP: 94111 ; COMPUTER READABLE FORM:
	HG .
	Two Embarcadero Center, 8th F n Francisco
	NDENCE ADDRESS: SEE: TOWNSEND and TOWNSEND and
	OF SECTION:
	L INFORMATION: ICANT: Ramer, J. Kevin
	<pre>seq_documentation_block: Sequence 7, Application US/08751512 Patent No. 6001962</pre>
	<pre>seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-751-512-7</pre>
	244 lAsnPheGluGluSerGlnThrPhePheGlyLeuTyrLysLeu 258
82 82	228 LeuThrSerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeuVa
22 77	211 hrThrGlyGlnMetTrpAlaArgSerSerTyrLeuGlyAlaValPheAsn ::: :::
21 72	194 STYPProGlnAspLeuValMetMetGluGlyLysMetMetSerTyrCysT :: ::
19 67	178 SerCysAsnAsnLeuProLeuSerHisLysValTyrMetArgAsnSerLy
17 62	161 snGluThrGlyLeuTyrPheValTyrSerLysValTyrPheArgGlyGln
16 57	144 yIleValLeuLeuSerGlyValLysTyrLysLysGlyGlyLeuValIleA ::: :::
14 52	128 GlyLysSerAsnSerArgSerMetProLeuGluTrpGluAspThrTyrGl ::: ::: :::
12 47	111 roSerProProGluLysLysGluLeuArgLysValAlaHisLeuThr
42	375 CACCAACCAAAGCCTTAAAGTATCATCTTTTGAAAAGCAAATAGCCAACC
11	111
11 37	101 MetPheGlnLeuPheHisLeuGlnLysGlu
10 32	84 euValMetPhePheMetValLeuValAlaLeuValGlyLeuGlyLeuGly
84	67 oLeuProProLeuLysLysArgGlyAsnHisSerThrGlyLeuCysLeuL
22	

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-09-508-849-1 x US-08-751-512-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS; LOCATION: 1..1128 US-08-751-512-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: MUTPHY, MAITHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02307K-07100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
573 CGAATACATG......CCAATGGAAC 592
                                                                                523 AGGGGGCTGGACTTCGCCTGTCTCGAGCATCACCATCACCATCACGAATT 572
                                                                                                                                                                     373 TTCAGCCACTTCGTGCCGGTCTTCCTGCCAGCGAAGCCCCACCACGACGCC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         423 AGCGCCGCGACCAACACCGGCGCCCCACCATCGCGTCGCAGCCCCTGT 472
                                                                                                                                                                                                                                                                                                                                                                                                                              323 AGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACTCCATCATGTAC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 CAAAACAAGCCCAAGGCGGCCGAGGGGCTGGACACCCAGCGGTTCTCGGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 CAAGAGGTTGGGGGACACCTTCGTCCTCACCCTGAGCGACTTCCGCCGAG 322
                                                                                                                                                                                                                                                                                               55 oProProProProProProLeuProProLeuProLeuProProLeuL 72
                                     86 tPhePheMetValLeuValAlaLeuValGlyLeuGlyLeuGlyMetPheG 103
                                                                                                                        79 ThrGlyLeu.....CysLeu...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/751,512 FILING DATE: 15-NOV-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
COMPUTER: I
                                                                                                                                                                                                                                                                                                                                                                       .....Pro.ProProProProProProLeuPr 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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4.168
60.606
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Gaps: 10
Percent Identity: 56.970
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

13-MAR-1996

US 08/614,584

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300
NFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 011823-006710US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)_576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 864 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1..
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                                                                                                                                                                                               ASDASDLeuProLeuSerHisLysValTyrMetArgAsDSerLysTyrPr 196
SerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeuValAsnPh
                                                                         lyGlnMetTrpAlaArgSerSerTyrLeuGlyAlaValPheAsnLeuThr 229
                                                                                                                                              OGlnAspLeuValMetMetGluGlyLysMetMetSerTyrCysThrThrG 213
                                                                                                                                                                                                                                                                     SerAsnSerArgSerMetProLeuGluTrpGluAspThrTyrGlyIleVa 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roProProGluLysLysGluLeuArgLysValAlaHisLeuThrGlyLys 129
                                                                                                                            CCAGGATCTGGTGATGATGGAGGGGAAGATGATGAGCTACTGCACTACTG
                                                                                                                                                                                                                                                                                                        hrGlyLeuTyrPheValTyrSerLysValTyrPheArgGlyGlnSerCys 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCCCTGAAAAAAAGGAGCTGAGGAAAGTGGCCCATTTAACAGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGATGCACACAGCATCATCTTTGGAGAAGCAAATAGGATCCCCCAGTC 424
                                                      GGCAGATGTGGGCCCGCAGCAGCTACCTGGGGGCAGTGTTCAATCTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                  TCCAACTCAAGGTCCATGCCTCTGGAATGGGAAGACACCTATGGAATTGT
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Ratio:
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5.144
87.151
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fusion protein"
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                  246
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aljgnment_block:
                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ US-08-855-825-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-855-825-13
                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                            US-09-508-849-1 x US-08-855-825-13
                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application Patent No. 6183951 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 eGluGluSerGlnThrPhePheGlyLeuTyrLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 GCCCAGCAGTGTCCTGCCTCTGCCTGGGCCTCGGTCCCTGCACCTG 124
                                       25 oProGlyThrValLeuProCysPro...ThrSerValProArgArgProG 41
                                                                                25 TCTCCTGCCCCATCTCCTTGGGCTGCCCGTGCTTCGTGCTTTGGACTACC 74
                                                                                                                       17 SerSerAlaSerSerProTrpAla.....Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/855,825
FILING DATE: 12-May-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taylor, Kent
Barry, Mary J.
TITLE OF INVENTION: Methods of Diagnosing Clinical Subtypes
of Crobin's Disease with Characteristic Responsiveness
Anti-Thl Cytokine Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P-PM 2591 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 780 base pairs
                                                                                                                                                                    to: US-08-855-825-13
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55.859
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                                                                                                                                                                                                                                                                        Percent Identity:
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Gaps:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08855825 Patent No. 6183951 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663 CACTCGATGTACCACGGGGCTGCGTTCCAGCTCACCCAGGGAGACCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 PheArgGlyGln......SerCysAsnAsnLeuProLe 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 CTCTCCTGGTCCCCACCAGTGGCATCTACTTCGTCTACTCCCAGGTGGTC 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 CACCACCT......GAACGTCTCTTCCTCCCAAGGGTGCGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 hrPhePheGlyLeuTyr 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 GGCCCAGGGGCTCCCTGGTGTTGGCCTCACACCTTCAGCTGCCCAGACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 lyGlnArgArgProProProProProProProPro..ProLeuProProP 57
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                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Plevy, Scott E.
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                                                                                                                                                                                                        TITLE OF
                ADDRESSEE:
                                                                                                              INVENTION: Methods of Diagnosing Clinical Subtypes
of Crohn's Disease with Characteristic
anti-Thi Cytokine Therapy
                                                                                                                                                                                                                                         Targan, Stephan R.
Taylor, Kent
Barry, Mary J.
                                                 ADDRESS:
    Campbell & Flores LLP
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LOCATION: 171..780

SEQUENCE DESCRIPTION: SEQUENCE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-855-825-11 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                     213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 ArgGlyAsnHisSerThrGlyLeuCysLeuLeuValMetPhePheMetVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 roProProProProLeuProProLeuProLeuProProLeuLysLys 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 lyGlnArgArgProProProProProProProPro..ProLeuProProP 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 oProGlyThrValLeuProCysPro...ThrSerValProArgArgProG 41
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AlaHisLeuThrGlyLysSerAsnSerArgSerMetProLeuGluTrpGl 140
                                                                                  CCCGTCAGCACCCCAAGATGCATCTTGCCCACAGCACCCTCAAACCTGCT
                                                                                                                                                   euGlnLysGluProSerProProProGluLysLysGluLeuArgLysVal 123
                                                                                                                                                                                                                                     GGCCCAGGGGCTCCCTGGTGTTGGCCTCACACCTTCAGCTGCCCAGACTG 312
                                                                                                                                                                                                                                                                                                                   lLeuValAlaLeuValGlyLeuGlyLeuGlyMetPheGlnLeuPheHisL 107
                                                                                                                                                                                                                                                                                                                                                                                                 ACCACCCTACACCTCCTCCTTCTGGGGCTGCTGCTGGTTCTGCTGCCTGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCCTGGATCCCCGGCCTGCCTGGGCCTTGGGTTCTCCCCATGA 174
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LENGTH: 780 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619)
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seq_documentation_block:
    Sequence 107, Application US/09166186A
    Patent No. 6080580
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 250
SEQ ID NO 107
LENGTH: 7208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Shanahan, William R.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (4527..4712,5225..5279,5457..5504,5799..6217)
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                     EATURE:
                      NAME/KEY:
                                              FEATURE:
                                                                                         NAME/KEY:
                                                                                                             FEATURE:
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LOCATION: (4713)..(5224)
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RRENT APPLICATION NUMBER: US/09/166,186A
FRENT FILING DATE: 1998-10-05
                                                                                                                              OCATION:
                                                                                                                                                                         EATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCCACCCACACAGATGGCATCCCCCACCTAGTCCTCAGCCCCTAGTACTG 762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCAGCTCCCAGAAGATGGTGTATCCAGGGCTGCAGGAACCCTGGCTG
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exon
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                                                                                                                              exon
(5225)..(5279)
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(5280)..(5456)
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alignment_block:
US-09-508-849-1 x US-09-166-186-107
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Percent Similarity:
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LOCATION: (5799)..(>6972)
PUBLICATION INFORMATION:
AUTHORS: Semon, D.
AUTHORS: Kawashima, E.
AUTHORS: Jongeneel, C.V.
AUTHORS: Shakhov, A.N.
AUTHORS: Nachopasov, S.A.
                                                                                                                                                                                                                                                                                                                                                     2197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE: Nucleotide sequence of the murine TNF locus, including the TITLE: TNF-alpha (tumor necrosis factor) and TNF-beta (lymphotoxin)genes JOURNAL: Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSUE: 21
PAGES: 9083-9084
DATE: 1987-11-11
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LOCATION: (5505)..(5798)
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                                        137 LeuGluTrpGlu...AspThrTyrGlyIleValLeuLeuSerGlyValLy 152
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CTGCTCTGGAGAGCAAGCACGGATCGTGCCTTTCTCCGACATGGCTTCTC 229:
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Percent Identity:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5,
                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
EILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2344
                            NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2494 AAGGACCGTGGGTGCGCTCAATGTACCAGGGGGCTGTGTTCCTGCTCAGT 2543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
                                                                       REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin. TITLE OF INVENTION: CYTOKINE TO SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTMARE: Microsoft Word, Version
URRENT APPLICATION DATA:
APPLICATION UMBER: US/08/670,354
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 51 0...
                                                                                                                                                                NAME: Anderson, Kathryn A. REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCCCCAGCAGTGTATTCTTTGGAGCCTTTGCACTG 2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eGluGluSerGlnThrPhePheGlyLeuTyrLysLeu 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGGAGACCAGCTGTCCACCCACACCGACGGCATCTCCCCATCTACACTT 2593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeuValAsnPh 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCATGTGCCTCTCCTCAGTGCGCAGAAGTCTGTGTATCCGGGACTTC 249:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCCCATCTACCTGGCACACGAGGTCCAGCTCTTTTCCTCCCAATACCC 2443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yrSerLysValTyrPheArgGlyGlnSerCysAsn........... 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sTyrLysLysGlyGlyLeuValIleAsnGluThrGlyLeuTyrPheValT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lyGlnMetTrpAlaArgSerSerTyrLeuGlyAlaValPheAsnLeuThr 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oGlnAspLeuValMetMetGluGlyLysMetMetSerTyrCysThrThrG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...AsnLeuProLeuSerHisLysValTyrMetArgAsnSerLysTyrPr 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTCCCAGGTGGTTTTCTCTGGAGAAAGCTGCTCCCCCAGGGCCATTCCC 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGAGCAACAACTCCCTCCTGATCCCCACCAGTGGCCTCTACTTTGTCT 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Application US/08670354 5763223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98103
CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WA
                                                     756822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kathryn A. Anderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine That Induces Apoptosis
                            5.
                                                                                                                                                 2835-B
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alignment_block:
US-09-508-849-1 x US-08-670-354-5
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; LOCATION:
US-08-670-354-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US96-10895-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 872 ATGGACCTGGATCAAGAAGCCAGCTTCTTTGGAGCCTTT 910
                                                                                                                                   822 AGCTAAAAAAAAATGACAGGATTTTTGTTTCTGTGACAAATGAACATTTG
                                                                                                                                                                                                                                                                                                         740 CTCATGAAGAGCGCCAGAAACAGC......TGTTGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                643 TGAAGACGCTTCCAAGATGGTCTCAAAGGACAAGGTGAGAACCAAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 sAsnAsnLeu.....ProL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543 CATTTCTCAACCACGTGCTCTTTAGGAATGGAGAGCTGGTCATCGAGCAG 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 alLeuLeuSerGlyValLysTyrLysLysGlyGlyLeuValIleAsnGlu 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 GACCTTAGGCCAGAAGATTGAATCCTGGGAGTCCTCTCGGAAAGGGCATT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 ATCACTCGGAGAAGCAACTCAGCTTTAATTCCAATCTCCAAGGATGGAAA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 CCTTGCCCAGAGGTGGAAGACCTCAGAAAGTGGCAGCTCACATTACTGGG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 ProProProGluLysLysGluLeuArgLys..ValAlaHisLeuThrGly 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                        772 CAGAGATGCCGAGTACGGACTGTACTCCATCTATCAGGGAGGATTGTTCG
                                                                                                                                                                                                                                                            217 aArg.....SerSerTyrLeuGlyAlaValPheA 227
                                                                                                                                                                                                                                                                                                                                               201 MetMetGluGlyLysMetMetSerTyrCysThrThrGlyGlnMetTrpAl 217
                                                                                                                                                                                                                                                                                                                                                                                                                                    184 euSerHisLysValTyrMetArgAsnSerLysTyrProGlnAspLeuVal 200
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                                                                                                                                                       snLeuThrSerAlaAspHisLeuTyrValAsnValSerGluLeuSerLeu ::||| ::: |||:::::: |||
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47..919
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59.444
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seq_documentation_block:

Sequence GENERAL

5, Application PC/TUS9610895 INFORMATION:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-508-849-1 x PCT-US96-10895-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 756822
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
493 GACCTTAGGCCAGAAGATTGAATCCTGGGAGTCCTCTCGGAAAGGGCATT 542
                                                                                                                                       443 ATCACTCGGAGAAGCAACTCAGCTTTAATTCCAATCTCCAAGGATGGAAA 492
                                                                                                                                                                                                                  129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: MUAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/548,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft WO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/FILING DATE: 25-JUN-1996 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Apple 7 SOPHWAY PROPERTY OF SOPHWAY PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                     ProProProGluLysLysGluLeuArgLys..ValAlaHisLeuThrGly 128
                                                                                                                                                                                                                                                                                 CCTTGCCCAGAGGTGGAAGACCTCAGAAAGTGGCAGCTCACATTACTGGG 442
                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                to: PCT-US96-10895-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Kathryn A. Anderso
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Microsoft Word, Version 6.0.1
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47..919
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1.748
59.444
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IBER: 32,172
NUMBER: 283
                                                               ......GluTrpGluAspThr...TyrGlyIleV 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 8
Percent Identity: 29.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2835-WO
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seq_documentation_block:
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693
                                                        FILING DATE: 23 DECEMBER ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Galibert, Laurent APPLICANT: Maraskovsky, Eugene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 AGCTAAAAAAAATGACAGGATTTTTGTTTCTGTGACAAATGAACATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 CTCATGAAGAGCGCCAGAAACAGC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 euSerHisLysValTyrMetArgAsnSerLysTyrProGlnAspLeuVal 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 GAGGGCCTGTATTACATCTATTCCCAAACATACTTCCGATTTCAGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 alLeuLeuSerGlyValLysTyrLysLysGlyGlyLeuValIleAsnGlu :::|||::: ||| :::::::||| ||||||||||:::::
                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 ValAsnPheGluGluSerGlnThrPhePheGlyLeuTyr 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               772 CAGAGATGCCGAGTACGGACTGTACTCCATCTATCAGGGAGGATTGTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 51 Unit CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Apple Operation
                                                                                                                                    APPLICATION NUMBER: USSN 08/813,509 FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                 APPLICATION NUMBER: USSN 60/
FILING DATE: 14 OCTOBER 1997
                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                       Perkins,
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                Microsoft
                 ns, Patricia Anne
NUMBER: 34,693
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22 DECEMBER 1997
                                                                              23 DECEMBER 1996
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                                                                                                                                                                                                                                                                                                                                                  Apple Operating System ft Word for Power Macint
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                                                                                               USSN 08/772,330
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2851-A
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120 euArgLysVal
342 TTCATGTAGGAGAATTAAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAAT 391
117LysLysGluL 120
292 GATTTTCAAGACACACTCTGGAGAGTCAAGATACAAAATTAATACCTGA 341
116 116
242 AAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCA 291
116 lu 116
101MetPheGlnLeuPheHisLeuGlnLysGluProSerProProProG 116 ::: ::: ::: ::: 192 CGCCCTGTTCTTCTATTTCAGAGCGCAGATGGATCCTAATAGAATATCAG 241
2 ATGTTCGTGGCCCTCCTGGGGCTGGGCTG
ValAlaLeuVal
.GCCGCCTCCC
73 ysArgGlyAsnHisSerThrGlyLeuCysLeuLeuValMetPhePheMet 89
ProProProProProProLeuProPr
40 roGlyGlnArgArgProProProProProProProProProLeu.ProPr 56
24 AlaProProGlyThrValLeuProCysProThrSerValProArgArg.P 40 ::: :::
lign seg 1/1 to: US-08-996-139-12 from: 1 to: 954
.ignment_block: /s-09-508-849-1 x US-08-996-139-12
ignment_scores: Quality: 185.00 Length: 342 Ratio: 1.294 Gaps: 14 ercent Similarity: 41.813 Percent Identity: 22.515
LOCATION: 1951 LOCATION: 1951
huRA
ORGANISM: Homo sapiens IMMEDIATE SOURCE:
POTHETICAL: N
NDEDNESS: si LOGY: linear
TYPE: nucleic acid
TELECOMMUNICATION INFORMATION:

	435	٠.
	13 E	٠. ٠.
	CATION DATA:	٠
	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25	٠. ٠.
	IBM PC compatible	٠. ٠.
	R READABLE FORM:	
	ZIP: 77010-3095	٠. ٠.
	: Texas	٠. ٠
	T: 130	٠
	ADDRESSEE: Thomas D. Paul	٠. ٠.
	R OF SEQUENCES: 14	
Ō	TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome	٠. ٠.
	: Warren, Stephe	٠.
		·. ·.
	CANT: Caskey,	•••
	_documentation_block: equence 1, Application US/07705490 atent No. 6107025 GENERAL INFORMATION:	seq.
	_name: /cgn2_6/ptodata/2/1na/6B_COMB.seg:US-07-705-490-1	seq_
	16 AIACITIGGGGCTITIAAAGIT 93	
	251 rPhePheGlyLeuTyrLysLeu 258 ::: ::: :::	
917	AACCCCTCCTTACTGGATCCGGATCAGGATGCAAC	
251	rLeuValAsnPheGluGluSerGlnTh	
234	221TyrLeuGlyAlaValPheAsnLeuThrSerAlaAspHisLeu ::: :: :::::::::::::::::::	
7.18	TAT	
· N	08 rTyrCysThrThrGlyGlnMetTrpAlaArgSerSer	
785	736 AGCATCAAAATCCCAAGTTCTCATACCCTGATGAAAGGAGGAAGCACCAA	
208		
735	::	
191		
181	164 yLeuTyrPheValTyrSerLysValTyrPheArgGlyGlnSerCysAsnA ::: ::::::::::::::::::::::::::::::	
635	TTTTAGCAATGGAAAACTAATAGTTAATCAGGATGG	
164	LysGlyGlyLeuValIleAsnGluThrGl	
585	536 CCCATAAAGTGAGTCTGTCCTCTTGGTACCATGATCGGGGTTGGGCCCAAG	
147	luTrpGluAspThrTyrGlyIleValLeu	
136 535	124AlaHisLeuThrGlyLysSerAsnSerArgSerMetPro	
491	442 GATGGCTCATGGTTAGATCTGGCCCAAGAGGAGCAAGCTTGAAGCTCAGCC	
123	123	

ATTORNEY/AGENT INFORMATION:

Paul, Thomas D.

32,714

D-5350

REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:

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seq_documentation_block:
   Sequence 1, Application US/07751891B
; Patent NO. 6180337
; GENERAL INFORMATION:
   APPLICANT: Caskey, C. T.
                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-07-751-891B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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LENGTH: 3765 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 GAACATCCTTTACAAATGCCTTGTAGAAAGCGCCATTGG.....AGCCC 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 713/651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 GGGAGCCCCCCCGAGAGGTGGGCTGCGGGCGCTCGAGGCCCAGCCGCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 CGCACTTCCACCACCACCTCCTCCATCTTCTTCTTCAGCCCCTGCTAGCGCC 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GlnGlnProPheAsnTyrProTyrProGlnIleTyrTrpValAspSerSe 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 713/
TELEX: 762829
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TOPOLOGY: lin
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                                                                               Fu, Ying-hui
TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
NUMBER OF SEQUENCES: 24
                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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CITY: Houston
                  STREET: 1301 McKinney, Suite 5100
                                       ADDRESSEE: Thomas D. Pau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO
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                                                                                                                                          Warren, Stephen T.
Oostra, Ben A.
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                                                                                                                                                                                  Pieretti, Maura
                                                                                                                                                                                                Nelson, David L.
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                          221 CGCACTTCCACCACCAGCTCCTCCATCTTCTTCAGCCCTGCTAGCGCC 172
                                                                                                                                                                              171 GGGAGCCCGCCCCGAGAGGTGGGCTGCGGGCGCTCGAGGCCCAGCCGCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 GAACATCCTTTACAAATGCCTTGTAGAAAGCGCCATTGG.....AGCCC 222
                                                                                    71
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21 CCTGGCACGGGC 10
                                     77 HisserThrGly 80
                                                                                                                            60 roProProLeuProLeuProLeuProProLeuLysLysArgGlyAsn 76
                                                                                                                                                                                                                                                                                                                                                                                                     18 rAlaSerSerProTrpAlaProProGlyThrValLeuProCys.ProThr 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GlnGlnProPheAsnTyrProTyrProGlnIleTyrTrpValAspSerSe 18
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COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/751,891B
FILING DATE: 29-Aug-1991
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                    CGCCTCCGCCGCCGCCGCCGCCGCCGCCGCCGCGCTGCCGCACGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: D-5350 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                      ....ProProProProProProProProLeuProProProProProP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 762829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Paul, Thomas D. REGISTRATION NUMBER: 32,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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Percent Identity: 46.591
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Maximum
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Sequence:
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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1411
1 MQQPFNYPYPQIYF
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Compugen
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 US-08-810-453-2
US-09-291-10A-2
US-09-290-640-25
PCT-US95-00362-2
PCT-US95-00362-5
US-08-649-100-9
US-08-649-100-9
US-08-630-172-5
US-08-630-172-5
US-08-630-172-21
PCT-US93-02475-13
US-08-855-825-14
US-08-855-825-14
US-08-855-825-12
US-08-855-825-12
US-08-855-825-12
US-08-912-227-4
US-08-912-227-3
US-08-93-02475-11
US-08-93-02475-11
US-08-93-02475-10
US-08-93-02475-10
US-08-93-02475-10
US-08-93-02475-10
US-08-93-02475-10
US-08-323-445A-10
US-08-313-903A-10
US-08-515-903A-10
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222.360 Million cell updates/sec
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Sequence 2, Appli sequence 25, Appli sequence 27, Appli sequence 27, Appli sequence 8, Appli sequence 17, Appli sequence 17, Appli sequence 17, Appli sequence 17, Appli sequence 11, Appli sequence 11, Appli sequence 12, Appli sequence 6, Appli sequence 6, Appli sequence 6, Appli sequence 10, Appli sequence 2, Appli sequence 2, Appli
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Query Match Best Local Similarity 91.8%; Matches 258; Conservative	RESULT 1 US-08-810-453-2 US-08-810-453-2 Sequence 2, Application US/0881045 Patent No. 5858990 GENERAL INFORMATION: FAS LIGAND TITLE OF INVENTION: PROLIFERAT NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: 2 CORRESPONDENCE ADDRESS: 2 COUNTRY: BOSTON STATE: MA COUNTRY: BOSTON STATE: MA COMPUTER EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER EADABLE: PC-DOS/MS- SOFTWARE: PATENTION ENGRAPTION: APPLICATION NUMBER: 36,637 REFERENCE/DOCKET NUMBER: 36,637 REFERENCE/DOCKET NUMBER: 31,637 REFERENCE/DOCK	•	28 178.5 12.7 233 5 29 178.5 12.7 233 6 30 176 12.5 16.3 6 31 175.5 12.4 281 3 31 175.5 12.4 281 3 34 175.5 12.4 281 3 35 175.5 12.4 281 5 36 175.5 12.4 281 5 37 175.5 12.4 281 5 38 173.5 12.4 281 5 39 172.5 12.4 281 5 39 172.5 12.2 233 152 6 40 170.5 12.1 152 3 41 166 11.8 158 1 42 166 11.8 158 1 43 164 11.6 158 1 44 164 11.6 158 1
Score 1389.5; DB 2; Pred. No. 2.8e-100; 0; Mismatches 0;	453 ATIVE DISORDERS ATIVE DISORDERS ATIVE DISORDERS ATIVE DISORDERS ATIVE DISORDERS FOR Atlantic Aversion #1.25 #1.0, Version #1.25 #1.10, Version #1.25	ALIGNMENTS	PCT-US95-12840-10 5422425-2 5175268-7 US-09-105-343A-7 US-08-670-354-2 US-08-684-031-1 US-08-883-086-10 PCT-US96-10895-2 5188969-1 PCT-US95-02475-2 US-08-883-086-6 US-08-883-086-6 US-08-883-086-6 US-08-937-470-10 US-07-794-400-11 US-07-794-400-12
Length 281; Indels 23; Gaps 1	TREATMENT OF		Sequence 10, Appl Patent No. 5472425 Patent No. 5175268 Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 15, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli

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APPLICATION NUMBER: US/08/815,190A
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
DEFERENCE/DOCKET NUMBER: 011823-006710US
                                                                                             Query Match
Best Local (
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                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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APPLICANT: Vasquez, Maximiliano
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CITY: Sa
STATE: C
COUNTRY:
                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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                         RSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 258
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                                                                                               Similarity
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Two Embarcadero
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der, William P.
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                                                                             Score 1389.5; DB 3;
Pred. No. 2.8e-100;
                                                                                                            DB 3;
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US-09-290-640-25
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CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
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Matches
                                                                                                                                      Sequence 2, Application PC/TUS9500362 GENERAL INFORMATION:
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                                                                         TITLE OF INVENTION: Ligand That Binds NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                          APPLICANT: IMMUNEX CORPORATION
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                               CITY:
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                                                             ADDRESSEE:
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              WA
                                            51 University
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                                            Immunex Corporation
University Street
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Pred. No. 2.8
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Mismatches
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                                                                                                                                                                                                                                                                 Sequence 5, Application PC/TUS9500362 GENERAL INFORMATION:
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                                                                                                                                                                                          TITLE OF INVENTION: LI
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 08/190,559
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APPLICATION NUMBER: PC
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FILING DATE: 07-JAN-1994
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
                                                                                                                                                    ADDRESSEE: Immunex Corporation STREET: 51 University Street
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SOFTWARE: Microsoft Word, Version 5.1a
                                                                                         COUNTRY: UZIP: 98101
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US-08-751-512-8
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COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Ramer, J. Kevin
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: Modified FAS Ligands
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                     CITY: San Francisco
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSYLGAVFNLTSADHLYVNISQLSLINFEESKTFFGLYKL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVINETGLYFVYSKVYFRGQSCNNQPLNHKVYMRNSKYPEDLVLMEEKRLNYFTTGQIWA 238
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Best Local Similarity 68.4%;
                                                                                                             ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD
                                                                                                                                                                                                                                                                                                                                              APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND A
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                      STREET: PO BOX 747
CITY: FALLS CHURCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 PPPPPPLPPPPPPPLPLPLPPLKKRGN------HSTGL---CL-----LVMFF 88
REGISTRATION
                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEESQTFFGLYKL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAKPTTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACLEHHHHHHEFEY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELCLVN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNNLPLS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08649100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy,
                                                                                                                                                                                                                                             ٧A
                                                                                                                                                                                                                                                                                                                                                                                               SHIRAKAWA, KAMON
MATUSUE, TOMOKAZU
NAGATA, SHIGEKAZU
CO, MAN SUNG
                                                                                                                                                                                                                                                                            E: BIRCH, STEWART, KOLASCH AND BIRCH PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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 NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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GERALD M
ER: 28,977
                                                                                    US/08/649,100
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Pred. No. 6.5e-57;
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                                                                                                                                                                                                                                                                                                                                                THE ANTI-FAS LIGAND ANTIBODY
                                                                                                                      #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: US-08-649-100-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
APPLICATION UNMBER: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: APPLe, Randolph T.
REGISTRATION NUMBER: 36,42
                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Relication Data:
CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 VMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNNLPLSHKVYMRNSKYPQDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111-3834
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TOPOLOGY: lir
TOPOLOGY:
                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6, Application US/08815190A 6046310
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              amino acid
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                               287 amino acids
                                                                               (415) 576-0300
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Schneider, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                (415)
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                                                                                                                                                                                                                                                                  11-MAR-1997
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                                                                                                576-0200
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                                                                                                                                                                                                                                                                                                                     Release #1.0, Version
                                                                                                                                                                                                                    US 08/614,584
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                                                                                                                                                36,429
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Sequence 17, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: ASSIGNMENTAL, AVI J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT FILLING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                         RESULT 10
US-08-630-172-5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-17
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                                                                                                                                                                            Sequence 5, Applic Patent No. 6060054
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Best Local Similarity 99.3%;
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.9%;
Best Local Similarity 87.2%;
Matches 156; Conservative
                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                 APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOV
TITLE OF INVENTION: LX
                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     121 SADHLYVNVSELSLVNFEESQTFFGLYKL 149
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                                                                                                      UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 230
                                                                                                                                                                                                                                                                                                                                                           170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 QLFHLQKELAELRESTSQMHTASSLEKQIGSPSPPPEKKELRKVAHLTGKSNSRSMPLEW 168
                                                                                                                                                                                                                                                                                                                               61
                             CITY: Denver
STATE: Colora
                                            ADDRESSEE: SHELL
            COUNTRY:
                                                                                                                                                                                                                                                                                                                          SKYYFRGQSCNNLPLSHKYYMRNSKYPQDLYMMEGKMMSYCTTGQMWARSSYLGAVFNLT 229
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80203
                                                                                                                                                                                           Application US/08630172
                             Colorado
          U.S.
                                                       Sheridan Ross & McIntosh
00 Lincoln Street, 35th Floor
                                                                                                                  NOVEL PRODUCT AND PROCESS FOR LYMPHOCYTE VETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 771.5; DB 3
Pred. No. 6.6e-53;
0; Mismatches 0
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Patent No. 6060054
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Staerz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2879

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOV
TITLE OF INVENTION: LXI
                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 FRGQSCNNLPLSHKYYMRNSKYPQDLYMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADH 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 PPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVY 173
                                                                                                                                                                                                                                                                                COUNTRY: U.S. ZIP: 80203
                                                                                                                                                                                                                                                                                                                    CITY: Denver
STATE: Colora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Connell, Gary J. REGISTRATION NUMBER: 32,020
                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRGQSCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYKGAVFNLTSADH 120
                                                                                                                                                                                                                                                                                                                  Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08630172
                                                                                                                                                                                                                                                                                                                                                   1700 Lincoln Street, 35th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                          Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514
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99.3%;
                                                                                                                 514
                                                                                                                                                                                                                                                                                                                                                                                                                                LYMPHOCYTE VETO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/630,172
                                                                                                                                               US/08/630,172
                                        2879-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 7e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2879-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 145;
                                                                                                                                                                                      #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-02475-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application PC/TUS9302475 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/85
FILING DATE: 12 MARCH 1992
ATTORNEY/AGENT INFORMATION:
NAME: Donald G. Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   TELEFAX: (619) 554-631 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: BJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19930412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 FRGQSCNNLPLSHKYYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADH 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 PPEKKELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 LYVNVSELSLVNFEESQTFFGLYKL 258
NAME/KEY: Lymphotoxin (murine)
OTHER INFORMATION: Two blank residues designated by
OTHER INFORMATION: "Yaa" are inserted after residue No. 4
OTHER INFORMATION: lymphotoxin and the sequence numbering
OTHER INFORMATION: by 2 starting with residue No. 5 in orc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DO SOFTWARE: Word Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 92122
                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                     ENGTH:
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                                                                                                                                                  i: 171 amino acids
AMINO ACIDS
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                                                                                                                                                                                                                        (619) 554-6312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Diskette,
VE System 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donald G.
                                                                                                                                                                                                                                        (619) 554-2421
                                                                                                               protein
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99.3%;
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                                                                                                                                                                                                                                                                                            28636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5 inch, 1.44 M storage
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                                                                                                                                                                                                                                                                               вл₩-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08855825 Patent No. 6183951 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                  INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION:
AUTHORS: Li, C-B., Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 GGLVINETGLYFVYSKYYFRGQSCN-----NLPLSHKYYMRNSKYPQDLVMMEGKMMSY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 GMFQLFHLQKEPSPPPEKK++--ELRKVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 PGLQGPWVRSMYQGAVFLLSKGDQLSTHTDGISHLHFSPSSVFFGAFAL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 CTTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: Cloning and Expression of Murine TITLE: Lymphotoxin cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 14.7%; Score 207; DB 5;
Local Similarity 31.4%; Pred. No. 2.7e-09;
hes 53; Conservative, 28; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 NSLLIPTSGLYFVYSQVVFSGESCSPRAIPTPIYLAHEVQLFSSQYPFHVPLLSAQKSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                  SEQUENCE CHARACTERISTICS:
                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Plevy, Scott E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVXXRFSAARTAHPLPQKHLTHGILKPAAHLVGYPSKQNSLLWRASTDRAFLRHGFSLSN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1987
                                                                                                                                                   NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/855,825
FILING DATE: 12-May-1997
                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4496-4501
                                                                        TELEFAX:
                  LENGTH: 203 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVENTION: Methods of Diagnosing Clinical Subtypes of Crohn's Disease with Characteristic Responsiveness to Anti-Th1 Cytokine Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                               San Diego
: California
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taylor, Kent
Barry, Mary J
                                                                        (619)
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                                                                          535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N 0
                                                                                                                                   P-PM 2591
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two blanks)
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US-08-855-825-14

MOLECULE TYPE: protein SEQ ID NO: 14:

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122 KVAHLTGKSNSRSMPLEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQ----

3 PPERLFLPRVRGTTLHLLLLGLLLVLLPGAQGLPGVGLTPSAAQTARQHPKMHLAHSTLK 62

63 PAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSP 122

64 PP--LPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKEPSPPPEKKELR 121

Matches Query Match

Local

l Similarity 56; Conserv

Conservative

13.48; 27.98;

Score 189; DB 4; 1 Pred. No. 7.9e-08; 4; Mismatches 103;

Length 203;

Indels

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US-08-912-227-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                    TELEFAX: 202-371-2
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
              MOLECULE TYPE:
                                                                                 SEQUENCE CHARACTERIST: ...: LENGTH: 205 amino acids
                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 16-AU
ATTORNEY/AGENT INFORM
                                                                                                                                                                                                                                                                                            CLASSIFICATION: 4: PRIOR APPLICATION DA:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
SOFTWARE: Patentir
CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Human Endokine Alpha NUMBER OF SEQUENCES: 10
                                                                                                                                                                        TELECOMMUNICATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 KATSSPLYLAHEVQLFSSQYPFHVPLLSSQKMVYPGLQEPWLHSMYHGAAFQLTQGDQLS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 --SCNNLPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQMWARSSYLGAVFNLTSADHLY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 THTDGIPHLVLSPSTVFFGAF 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 VNVSELSLVNFEESQTFFGLY 256
                               TOPOLOGY:
                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER FILING DATE: Here
                                                                                                                                                                                                         NAME: Steffe, Eric
REGISTRATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                TELEPHONE:
                                                                                                                                                                                            REFERENCE/DOCKET NU
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              protein
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NW, SUITE 600
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Query Match

13.3%;

Score 187;

DB 2:

Length 205

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64 PP--LPLPPLKKRGNHSTGLCLLVMFFMVLVALVGLGLGMFQLFHLQKEPSPPPEKKELR 121

3 PPERLFLPRVCGTTLHLLLLGLLLVLLPGAQGLPGVGLTPSAAQTARQHPKMHLAHSTLK 62

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              Query Match
Best Local
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 Matches
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                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                              MOLECULE TYPE:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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OPERATING SYSTEM:
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                                                                                                             TOPOLOGY:
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ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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                Similarity
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28.1%;
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   33;
              Score 187; DB 4; Length 205 Pred. No. 1.1e-07;
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